

XX New compound for diagnosing or treating inflammatory disorders, e.g.
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.

XX Claim 6; Page 23; 37pp; English.

CC The invention describes an anti-inflammatory compound comprising (I). The
 CC compound is useful for diagnosing or treating inflammatory disorders,
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.,
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFKB) essential modulator (NEMO).

SQ Sequence 6 AA;

Query	1 ADWSWA 6	Score 40;	DB 6;	Length 6;
Best Local Similarity	100.0%;	Pred. No.	1.4e+06;	
Matches	6;	Conservative	0;	Mismatches 0;
Db	1 ADWSWA 6	Indels 0;	Gaps 0;	

RESULT 4
 ADA61846
 ID ADA61846 Standard; peptide; 6 AA.

XX
 XX
 AC ADA61846;
 XX
 DT 20-NOV-2003 (first entry)

DB NFKB essential modulator (NEMO) binding Peptide #46.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis;
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 KW systemic lupus erythematosus; multiple sclerosis; transplant rejection;
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 KW necrosis factor kappa B essential modulator.

XX Unidentified.

XX
 XX
 PN US2003054999-A1.

XX
 XX
 PD 20-MAR-2003.

XX
 XX
 PP 02-MAY-2001; 2001US-00847946.

XX
 XX
 PR 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00641260.

XX
 PA (PRAE-) PRACTIS PHARM INC.
 PA (UYYA) UNIV VALE.

XX
 PT May MJ, Ghosh S, Findeis MA, Phillips K;

XX
 DR WPI; 2002-121889/16.

XX
 PT Novel antiinflammatory compound comprising membrane translocation domain
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
 PT activation, and for treating asthma, lung inflammation, psoriasis.

XX
 PS Claim 6; Page 62; 88pp; English.

XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AM48528-AM48545), comprising a membrane translocation domain (AM48620-
 CC AM48627 or AM48645-AM48651) which comprises from 6-15 amino acid
 residues, fused to a NEMO binding sequence (AM48525-AM48619). The
 CC antiinflammatory compounds have antiasthmatic, cytostatic, nootropic,
 CC antiarthritic, osteopathic, antibacterial, antipsoriatic, antirheumatic,

Q	Q	immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IkappaB) at the NEMO domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
Q	Sequence 7 AA;	
Y		Query Match Best Local Similarity 100.0%; Score 40; DB 5; Length 7; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
b	1 ADWSWA 6	1 ADWSWA 6
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X	DA61850 Standard; peptide; 7 AA.	
X	ADA61850;	
X	20-NOV-2003 (first entry)	
X	NFKB essential modulator (NEMO) binding peptide #50.	
X	NEMO binding domain; NBD; I kappa B kinase beta; IKbeta; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antibacterial; immunosuppressive; dermatological; neuroprotective; cytostatic; nortropic; virucide; gene therapy; anti-inflammatory; inflammatory disorder; asthma; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; sepsis; vasculitis; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis; Alzheimer's disease; viral infection; NF-kappa B essential modulator; necrosis factor kappa B essential modulator.	
X	Unidentified.	
X	US2003054999-A1.	
D	20-MAR-2003.	
D	02-MAY-2001; 2001US-00847946.	
D	02-MAY-2000; 2000US-0201261P.	
A	(MAYM/) MAY M J.	
A	(GROS/) GHOSH S.	
A	(FIND/) FINEIS M A.	
A	(PHIL/) PHILLIPS K.	
A	(HANN/) HANNIG G.	
I	May MJ, Ghosh S, Fineis MA, Phillips K, Hannig G;	
R	WPI; 2003-596541/56.	
R	New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.	

CC antiatherosclerotic, virucide and antiallergic activity. The compounds
 CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
 CC domain that results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
 CC viral infections; and ataxia telangiectasia. The compounds are also
 CC useful for treating pro-inflammatory responses such as allergies,
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
 CC sunburn, aging and arthritis

SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 5; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6

Db 1 ADWSWA 6

RESULT 8

Qy 1 ADWSWA 6
ID ADAM48567
XX 1 ADWSWA 6

RESULT 8

Qy 1 ADWSWA 6
ID ADAM48567
XX 1 ADWSWA 6

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 70.

XX antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KW ataxia telangiectasia; allergy; anaphylaxis; arthritis;

XX OS Synthetic.

PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PR 02-MAY-2001; 2001WO-US014346.

XX PR 02-MAY-2000; 2000US-0201261P.

XX PR 22-AUG-2000; 2000US-00643260.

XX PA (PRAE-) PRECIS PHARM INC.

XX PA (UYA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
 PT activation, and for treating asthma, lung inflammation, psoriasis.

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AM48628-AM48645), comprising a membrane translocation domain (AM48620-
 CC AM48627 or AM48646-AM48651) which comprises from 6-15 amino acid

residues, fused to a NEMO binding sequence (AM48525-AM48619). The

antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

anticancer, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic,

antiatherosclerotic, virucide and antiallergic activity. The compounds

act as selective inhibitors of cytokine-mediated NFkappaB activation by

blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

domain that results in inhibition of IKKbeta kinase activation and

subsequent decreased phosphorylation of IkappaB. The compounds are useful

for treating inflammatory disorders, e.g. asthma, lung inflammation or

cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;

CC viral infections, and ataxia telangiectasia. The compounds are also

useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis drug or food sensitivity, eczema, dermatitis,

CC sunburn, aging and arthritis

SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 5; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6

Db 3 ADWSWA 8

RESULT 9

Qy 1 ADWSWA 6
ID ADA61851
XX 1 ADWSWA 8

DT 20-NOV-2003 (first entry)

DE NFKB essential modulator (NEMO) binding peptide #51.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta; cancer;

KW antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic;

KW antiinflammatory; antiasthmatic; antibacterial; immunosuppressive;

KW antiarthritic; osteopathic; neuroprotective; cytostatic; nootropic; virucide;

KW dermatological; neuroprotective; inflammatory disorder; asthma;

KW gene therapy; anti-inflammatory; psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

XX OS Unidentified.

PN US2003054999-A1.

XX PD 20-MAR-2003.

XX PR 02-MAY-2001; 2001US-00847946.

XX PR 02-MAY-2000; 2000US-0201261P.

XX PR (MAYM) MAY M J.

PA (GHOS) GHOSH S.

PA (FIND) FINDEIS M A.

PA (PHIL) PHILLIPS K.

PA (HANN) HANNIG G.

XX

PR May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX DR WPI; 2003-59651/56.

XX PT New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.
 XX
 PS Claim 6; Page 23; 37pp; English.
 XX
 CC The invention describes an anti-inflammatory compound comprising (I). The
 compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates, an anti-inflammatory peptide that binds to, and down-regulates, a necrosis factor kappa B (NFKB) essential modulator (NEMO).
 CC
 CC necrosis factor kappa B (NFKB) essential modulator (NEMO).
 CC
 XX Sequence 8 AA;

Qy	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	1 ADWSWA 6	100.0%	DB 6;	Length 8;	Best Local Similarity 100.0%;	Pred. No.	1.4e+06;	0;	0;	0;
Db	1 ADWSWA 6				Matches 6;	Conservative		0;	0;	0;

RESULT 10
 ADA61943
 ID ADA61943 standard; peptide; 8 AA.
 XX
 AC ADA61943;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DR NFKB essential modulator (NEMO) binding peptide #43.
 XX
 KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatologic; neuroprotective; cytostatic; nootropic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; sepsis; vasculitis; autoimmune disease;
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 KW Alzheimer's disease; viral infection; NF kappa B essential modulator;
 KW necrosis factor kappa B essential modulator;
 XX
 OS Unidentified.
 XX
 PN US2003054999-A1.
 XX
 PD 20-MAR-2003.
 XX
 PP 02-MAY-2001; 2001US-00847946.
 XX
 PR 02-MAY-2000; 2000US-0201261P.
 XX
 PR 22-AUG-2000; 2000US-00643260.
 XX
 PR (PRAE-) PRABCIS PHARM INC.
 PR (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.

XX
 PA (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 PA (FIND/) FINDEIS M A.
 PA (PHIL/) PHILLIPS K.
 PA (HANN/) HANNIG G.
 XX
 PR 02-MAY-2000; 2000US-0201261P.
 XX
 PR Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappa B activation, and for treating asthma, lung inflammation, psoriasis.
 PT
 PT
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC ARM48627 or ARM48646-ARM48651) which comprises from 6-15 amino acid
 CC residues, fused to a NEMO binding sequence (ARM48525-ARM48619). The
 CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
 CC antiarthritic, osteopathic, antibacterial, nootropic, immunosuppressive,
 CC antiatherosclerotic, virucide and antiallergic activity. The compounds
 CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
 CC domain that results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
 CC viral infections; and ataxia telangiectasia. The compounds are also
 CC useful for treating pro-inflammatory responses such as allergies,
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
 CC sunburn, aging and arthritis

XX Sequence 9 AA:

Query Match 100.0%; Score 40; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 ID AM48566
 Db 2 ADWSWA 7

RESULT 12

XX Anti-inflammatory peptide SEQ ID NO 69.

DE AM48566
 ID AM48566 standard; peptide; 9 AA.

XX AC AM48566;
 DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 69.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antiphoriatic; nootropic;
 KW antiarthritic; antiasthmatic; osteopathic; antibacterial; viricide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiinflammatory; dermatological; antiatherosclerotic; nootropic;
 KW antiinflammatory; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PP 02-MAY-2001; 2001WO-US014346.

XX PR 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRACIS PHARM INC.

PA (UYA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain
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 PT activation, and for treating asthma, lung inflammation, psoriasis.

XX PS Claim 6; Page 62; 88pp; English.

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 CC AM48528-AM48645), comprising a membrane translocation domain (AM48620-
 CC AM48627 or AM48646-AM48651) which comprises from 6-15 amino acid
 CC residues, fused to a NEMO binding sequence (AM48525-AM48619). The
 CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antirheumatic, antiarthritic, osteopathic, antibacterial,
 CC immunosuppressive, dermatological, neuroprotective, nootropic,
 CC antiatherosclerotic, viricide and antiallergic activity. The compounds
 CC act as selective inhibitors of cytokine-mediated NkappaB activation by
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
 CC domain that results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
 CC viral infections; and ataxia telangiectasia. The compounds are also
 CC useful for treating pro-inflammatory responses such as allergies,
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
 CC sunburn, aging and arthritis

XX Sequence 9 AA:

Query Match 100.0%; Score 40; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 ID AM48569
 Db 1 ADWSWA 6

RESULT 13

XX Anti-inflammatory peptide SEQ ID NO 69.

XX AC AM48569;
 DT 20-MAR-2002 (first entry)

XX DS Anti-inflammatory peptide SEQ ID NO 72.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antiarthritic; antiasthmatic; osteopathic; antibacterial; viricide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiinflammatory; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PR 02-MAY-2001; 2001WO-US014346.

XX PR 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

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PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX DR WPI; 2003-596541/56.
XX PT New compound for diagnosing or treating inflammatory disorders, e.g. PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or PT cancer, comprises a membrane translocation domain and a NEMO binding PT sequence.
XX PS Claim 6; Page 23; 37pp; English.
XX CC The invention describes an anti-inflammatory compound comprising (I). The CC compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, CC Alzheimer's disease or viral infection. This is the amino acid sequence CC of an anti-inflammatory peptide that binds to, and down-regulates, CC necrosis factor kappa B (NFKB) essential modulator (NEMO).
XX SQ sequence 9 AA;

Query Match 100.0%; Score 40; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWA 6
| | | | |
Db 3 ADWSWA 8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 26, 2004, 13:08:54 ; Search time 42 Seconds
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Title: US-09-847-940C-6
 Perfect score: 40
 Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
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Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

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 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1
 US-09-847-946A-41
 Sequence 41, Application US/09847946A
 Publication No. US20030054999A1
 GENERAL INFORMATION:
 APPLICANT: May, Michael J
 APPLICANT: Ghosh, Sankar
 APPLICANT: Fideis, Mark A
 APPLICANT: Phillips, Kathryn
 APPLICANT: Hanning, Gerhard
 TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 FILE REFERENCE: PPI-119
 CURRENT APPLICATION NUMBER: US/09/847-946A
 CURRENT FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: 60/201,261
 PRIOR FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: 09/643,260
 PRIOR FILING DATE: 2000-08-22
 NUMBER OF SEQ ID NOS: 160

SEQUENCES

Result No.	Score	Query Length	DB ID	Description
1	40	100.0	6	US-09-847-946A-41 Sequence 41, Appl Sequence 73, Appl
2	40	100.0	6	US-09-847-946A-73 Sequence 77, Appl
3	40	100.0	7	US-09-847-946A-77 Sequence 77, Appl
4	40	100.0	8	US-09-847-946A-70 Sequence 78, Appl
5	40	100.0	8	US-09-847-946A-78 Sequence 78, Appl
6	40	100.0	9	US-09-847-946A-69 Sequence 69, Appl
7	40	100.0	9	US-09-847-946A-72 Sequence 72, Appl
8	40	100.0	9	US-09-847-946A-75 Sequence 75, Appl
9	40	100.0	9	US-09-847-946A-76 Sequence 76, Appl
10	40	100.0	10	US-09-847-946A-71 Sequence 71, Appl
11	40	100.0	10	US-09-847-946A-74 Sequence 74, Appl
12	40	100.0	11	US-09-847-946A-68 Sequence 68, Appl
13	37	92.5	12	US-10-441-625-17 Sequence 17, Appl
14	37	92.5	13	US-10-441-626-17 Sequence 17, Appl
15	37	92.5	14	US-10-441-626-17 Sequence 17, Appl
16	37	92.5	15	US-10-282-122A-43572 Sequence 43572, Appl
17	36	90.0	6	US-09-847-940B-4 Sequence 4, Appl
18	36	90.0	9	US-09-847-940B-5 Sequence 5, Appl
19	36	90.0	10	US-09-847-946A-4 Sequence 4, Appl
20	36	90.0	10	US-09-847-946A-5 Sequence 5, Appl
21	36	90.0	6	US-09-847-946A-39 Sequence 39, Appl
22	36	90.0	6	US-09-847-946A-40 Sequence 40, Appl
23	36	90.0	6	US-09-847-946A-51 Sequence 51, Appl
24	36	90.0	6	US-09-847-946A-62 Sequence 62, Appl
25	36	90.0	7	US-09-847-946A-55 Sequence 55, Appl
26	36	90.0	7	US-09-847-946A-66 Sequence 66, Appl
27	36	90.0	8	US-09-847-946A-48 Sequence 48, Appl
28	36	90.0	8	US-09-847-946A-56 Sequence 56, Appl
29	36	90.0	8	US-09-847-946A-59 Sequence 59, Appl
30	36	90.0	9	US-09-847-946A-67 Sequence 67, Appl
31	36	90.0	9	US-09-847-946A-69 Sequence 69, Appl
32	36	90.0	9	US-09-847-946A-50 Sequence 50, Appl
33	36	90.0	9	US-09-847-946A-53 Sequence 53, Appl
34	36	90.0	9	US-09-847-946A-54 Sequence 54, Appl
35	36	90.0	9	US-09-847-946A-58 Sequence 58, Appl
36	36	90.0	9	US-09-847-946A-61 Sequence 61, Appl
37	36	90.0	9	US-09-847-946A-64 Sequence 64, Appl
38	36	90.0	9	US-09-847-946A-65 Sequence 65, Appl
39	36	90.0	10	US-09-847-946A-49 Sequence 49, Appl
40	36	90.0	10	US-09-847-946A-52 Sequence 52, Appl
41	36	90.0	10	US-09-847-946A-57 Sequence 57, Appl
42	36	90.0	10	US-09-847-946A-60 Sequence 60, Appl
43	36	90.0	10	US-09-847-946A-63 Sequence 63, Appl
44	36	90.0	11	US-09-847-946A-46 Sequence 46, Appl
45	36	90.0	147	US-10-424-599-199086 Sequence 199086,

ALIGNMENTS

RESULT 2
US-09-847-946A-73
; Sequence 73, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; CURRENT FILING DATE: 2001-05-02
; PRIORITY NUMBER: 60/201, 261
; PRIORITY APPLICATION NUMBER: 09/643, 260
; PRIORITY FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 73
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-73

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
Db 1 ADMSWA 6

RESULT 3
US-09-847-946A-77
; Sequence 77, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; CURRENT FILING DATE: 2001-05-02
; PRIORITY NUMBER: 60/201, 261
; PRIORITY FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-77

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
Db 3 ADMSWA 8

RESULT 5
US-09-847-946A-78
; Sequence 78, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; CURRENT FILING DATE: 2001-05-02
; PRIORITY NUMBER: 60/201, 261
; PRIORITY FILING DATE: 2000-08-22
; PRIORITY APPLICATION NUMBER: 09/643, 260
; PRIORITY FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 77
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-77

Query Match 100.0%; Score 40; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
Db 1 ADMSWA 6

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 6
US-09-847-946A-69
; Sequence 69, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643, 260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-69

Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06; DB 10; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 7
US-09-847-946A-72
; Sequence 72, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-75

Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06; DB 10; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 3 ADWSWA 8

RESULT 8
US-09-847-946A-75
; Sequence 75, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-72

Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06; DB 10; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 9
US-09-847-946A-76
; Sequence 76, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: Sequence
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence
; US-09-847-946A-76

Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 ADWSWA 6	
Db	2 ADWSWA 7	

RESULT 10
US-09-847-946A-71
Sequence 71, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 71
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence

Query Match 100.0%; Score 40; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 ADWSWA 6	
Db	2 ADWSWA 7	

RESULT 11
US-09-847-946A-74
Sequence 74, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hanning, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 74
LENGTH: 10
TYPE: PRT

RESULT 12
US-09-847-946A-68
Sequence 68, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hanning, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 68
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence

Query Match 100.0%; Score 40; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 ADWSWA 6	
Db	3 ADWSWA 8	

RESULT 13
US-10-441-625-17
Sequence 17, Application US/10441625
Publication No. US20030203467A1
GENERAL INFORMATION:
APPLICANT: Gualfetti, Peter
APPLICANT: Mitchinson, Colin
APPLICANT: Phillips, Jay Ian
TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
TITLE OF INVENTION: Compositions
FILE REFERENCE: GC631
CURRENT APPLICATION NUMBER: US/10/441,625
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 17
LENGTH: 236
TYPE: PRT
ORGANISM: Gliocladium roseum (3)
US-10-441-625-17

Query Match 92.5%; Score 37; DB 12; Length 236;
 Best Local Similarity 83.3%; Pred. No. 5 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy. 1 ADWSWA 6
 Db 63 ADWSWS 68

RESULT 14
 US-10-441-626-17
 Sequence 17, Application US/10441626
 Publication No. US20030186418A1
 GENERAL INFORMATION:
 APPLICANT: Guilletti, Peter
 APPLICANT: Hutchinson, Colin
 APPLICANT: Phillips, Jay Ian
 TITLE OF INVENTION: No. US20030186418A1el Variant EGII-Like Cellulase
 TITLE OF INVENTION: Compositions
 FILE REFERENCE: GC631
 CURRENT APPLICATION NUMBER: US/10/441,626
 CURRENT FILING DATE: 2003-05-19.
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 17
 LENGTH: 236
 TYPE: PRT
 ORGANISM: *Glacioladium roseum* (3)
 US-10-441-626-17

Query Match 92.5%; Score 37; DB 14; Length 236;
 Best Local Similarity 83.3%; Pred. No. 5 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy. 1 ADWSWA 6
 Db 63 ADWSWS 68

RESULT 15
 US-09-815-242-5090
 Sequence 5090, Application US/09815242.
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 PROKARYOTES
 FILE REFERENCE: BILTRA.01A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 5090
 LENGTH: 885
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-815-242-5090

Query Match 92.5%; Score 37; DB 9; Length 885;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy. 1 ADWSWA 6
 Db 563 ADWAWA 568

Search completed: April 26, 2004, 13:14:32
 Job time : 42 secs

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RESULT 2		SEQUENCE		SQ	
Q8G659;	PRELIMINARY;	PRT;	274 AA.	SEQUENCE	375 AA; 41862 MW; EC9A1D744C56056E CRC64;
ID				Query Match	92.5%; Score 37; DB 5; Length 375;
AC	Q8G659;			Best Local Similarity	83.3%; Pred. No. 3.6e-02;
DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)			Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)			OY	1 ADMSWA 6 :
DE	Probable dihydroorotate dehydrogenase electron transfer subunit.			Db	46 SDMSWA 51
GN	PYRK OR BL0790.				
OS	Bifidobacterium longum.				
OC	Bacteria; Actinobacteria; Actinomycetales; Bifidobacteriales;				
OC	Bifidobacteriaceae; Bifidobacterium.				
OX	NCBI_TaxID:216816;				
RN					
[1] SEQUENCE FROM N.A.					
RP					
RC	STRAIN=NCC 2705;				
RX	MEDLINE=22394977; PubMed=12381807;				
RA	Schein M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,				
RA	Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,				
RA	Pridmore R.D., Arigoni F., The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 99:14422-14427 (2002).				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).				
DR	EMLB; AE014701; AAN2405.1; -.				
DR	GO; GO:0014491; F:oxidoreductase activity; IEA.				
DR	GO; GO:005118; P:electron transport; IEA.				
DR	InterPro; IPR008333; FAD_binding_6; 1.				
DR	Pfam; PF00070; FAD_binding_6; 1.				
KW	Complete proteome.				
SQ	274 AA; 971E0016E79636DB CRC64;				
RP					
RC	SEQUENCE FROM N.A.				
RX	STRAIN=1021;				
RA	MEDLINE=21396507; PubMed=11481430;				
RA	Capela, D., Barloy-Hubler, F., Gouzy, J., Bothé, G., Ampe, F., Batut, J., Boistard, D., Becker, A., Boultry, M., Cadieu, E., Dreano, S., Gloux, S., Godrie, T., Goffeau, A., Kahn, D., Kiss, E., Lejaire, V., Masuy, D., Pohl, T., Portetelle, D., Puehler, A., Purnelle, B., Ramsperger, U., Renard, C., Thebault, P., Vandebol, M., Weidner, S., Galibert, F.; "Analysis of the chromosome sequence of the legume symbiont <i>Sinorhizobium meliloti</i> strain 1021." <i>Proc. Natl. Acad. Sci. U.S.A.</i> 98:9877-9882 (2001).				
RA	EMLB; AL591790; CAC6862.1; -.				
RA	Hypothetical protein; Complete proteome.				
RX	SEQUENCE 437 AA; 48372 MW; 950E0B3DA963CE78 CRC64;				
RA	Best Local Similarity 83.3%; Pred. No. 4.2e+02;				
RA	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
OY	1 ADMSWA 6 :				
Db	171 ADMSWA 176				
RESULT 3					
Q86K50	PRELIMINARY;	PRT;	375 AA.		
AC	Q86K50;				
DT	01-JUN-2003 (TREMBrel. 24, Created)				
DT	01-JUN-2003 (TREMBrel. 24, Last sequence update)				
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)				
DB	Hypothetical protein.				
OS	Dictyostelium discoideum (Slime mold).				
OC	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.				
OX	NCBI_TaxID:44689;				
RN					
SEQUENCE FROM N.A.					
RP					
RC	SEQUENCE FROM N.A.				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	11				
RN	SEQUENCE FROM N.A.				
RP					
RC	SEQUENCE FROM N.A.				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	12				
RN	SEQUENCE FROM N.A.				
RP					
RC	SEQUENCE FROM N.A.				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	13				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	14				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	15				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	16				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	17				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	18				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	19				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	20				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	21				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	22				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	23				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	24				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	25				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	26				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	27				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	28				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	29				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	30				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	31				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	32				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	33				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	34				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	35				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	36				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	37				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	38				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	39				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of chromosome 2 of <i>Dictyostelium discoideum</i> ." <i>Nature</i> 418:79-85 (2002).				
RA	40				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner, G., Eichinger, L., Szaranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A., Noegel, A. A.; "Sequence analysis of				

QY 1 ADWSWA 6
Db 158 SWWSWA 163

RESULT 8

ID 086712; PRELIMINARY; PRT; 610 AA.

AC 086712;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DB Hypothetical protein SCO6530.

GN SCO6530 OR SC5C71_15;

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinomycetida; Actinomycetales;
Streptomyces; Streptomyctaceae; Streptomyces.

OC NCBI_TaxID=1902;

OX NCBI_TaxID=1902;

RN [1]
SEQUENCE FROM N.A.

RC STRAIN=A3 (2) / M145;
MEDLINE=21596410; PubMed=12000953;

RA Bentley S.P., Chater K.F., Cerdeño-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., O'Gail M.A., Kieser H.,
Riley D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser F., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Laike L., Murphy L., Oliver K., O'Neill S.,
Rabinowitzsch E., Raiandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3 (2)." ;
RL Nature 417:11-147 (2002).

DR EMBL; AL939128; CAA20271.1; -.

DR PIR; T35222; T35222.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 610 AA; 67368 MW;

Query Match 92.5%; Score 37; DB 16; Length 610;
Best Local Similarity 83.3%; Pred. No. 5.9e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 83 ADWAWA 88

RESULT 9

ID 091389; PRELIMINARY; PRT; 885 AA.

AC 091389;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE Two-component sensor KdpD.

GN KDPD OR PA636.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

OC NCBI_TaxID=287;

RN [1]
SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PA01;
MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Brinkman F.S.L., Michelotti S.D., Warren P.M.,
Oxman A.J., Brown A.L., Mizoguchi S.D., Warren P.M.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalki D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.,
"Complete genome sequence of Pseudomonas aeruginosa PA01, an

RT opportunistic pathogen.";
RL Nature 406:959-964 (2000);
CC -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
DR EMBL; AE004591; AAG05025.1; -.
DR PIR; C83441; C83441.
DR HSSP; P02233; IJOY.

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR GO; GO:0077600; P:sensory perception; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR03594; ATPbind ATPase.
DR InterPro; IPR04358; Bact_sens_pr_C.
DR InterPro; IPR03018; GAF.
DR InterPro; IPR05467; His kinase.
DR InterPro; IPR03661; His_kinA_N.
DR InterPro; IPR03582; KdpD.
DR InterPro; IPR03582; KdpD; Usp dom.
DR Pfam; PF00512; HisPAc_C; 1.
DR Pfam; PF00512; HisKA; 1.
DR Pfam; PF00582; Usp; 1.
DR PRINTS; PRO034; BCTRLSENSOR.
DR PRODOM; P0011725; KdpD; 1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HisPAc_C; 1.
DR SMART; SM03388; HisKA; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase;
KW Complete proteome.

SQ SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;
Best Local Similarity 83.3%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 563 ADWAWA 568

RESULT 10

ID 0825E1; PRELIMINARY; PRT; 173 AA.

AC 0825E1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN SAV7517.

OS Streptomyces avermitilis.

OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
Streptomyces; Streptomyctaceae; Streptomyces.

OC NCBI_TaxID=33903;

RN [1]
SEQUENCE FROM N.A.

RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11573948;

RA Ikeda H., Ishikawa J., Hamamoto A., Takahashi C.,
Omura S., Ikeda H., Ishikawa J., Hamamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
Kikuchi H., Shiba T., Sakai Y., Hattori M.,
"Genome sequence of an industrial microorganism Streptomyces
avermiculicib; deducing the ability of producing secondary
metabolites";
RT metabolites";
RT RUE; GO:000511; F:ATP binding; IEA.
RN [2]
SEQUENCE FROM N.A.

RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22408306; PubMed=12693562;

RA Ikeda H., Ishikawa J., Hamamoto A., Shinose M., Kikuchi H., Shiba T.,

RA	Sakaki Y., Hattori M., Omura S.;	RN	[1]
RT	"Complete genome sequence and comparative analysis of the industrial	RP	SEQUENCE FROM N.A.
RT	microorganism Streptomyces avermitilis."	RC	TISSUE-Brain;
RL	Nat. Biotechnol. 21:526-531(2003).	RA	Strausberg R.;
DR	EMBL: AP00050; BAC7228.1; -.	RC	Submitted (Nov-2002) to the EMBL/GenBank/DDBJ databases.
SQ	SEQUENCE 173 AA; 18912 MW; 22B26CTD222CA60 CRC64;	DR	EMBL: BC04173; AAH40173.1; -.
Query Match 90.0%; Score 36; DB 16; Length 173;	KW	Hypothetical protein.	
Best Local Similarity 83.3%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	SQ	SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;	
OY 1 ADMSWA 6	OY	Query Match 90.0%; Score 36; DB 4; Length 227;	
Db 53 ADMSWA 58	OY	Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 11	Db	113 ADMSW 117	
O9ACRS			
ID O9ACRS	PRELIMINARY;	PRT;	205 AA.
AC			
DT 01-JUN-2001 (TREMBrel. 17, Created)	ID	O7YGUB	PRELIMINARY;
DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)	AC	O7YGUB	PRELIMINARY;
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)	DT	01-OCT-2003 (TREMBrel. 25, Created)	
DE Hypothetical protein SCPI-253.	DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)	
GN SCPI-253.	DE	Cytochrome oxidase subunit II.	
OS Streptomyces coelicolor.	OS	Sphendon punctatus (Hattoria) (Tuatara).	
OG Plasmid SCPI.	OG	Mitochondrion.	
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetales;	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Streptomyces; Streptomycetaceae; Streptomyces.	OC	lepidosauia; Sphenodontia; Sphenodontidae; Sphenodon.	
OX NCBI_TAXID=1902;	OX	NCBI_TAXID=8508;	
RN [1]	RN	SEQUENCE FROM N.A.	
RP			
RC			
STRAIN=A3(2);	RP	SEQUENCE FROM N.A.	
MLINDBE=21996410; PubMed=12000953;	RA	Rest J.S., Ast J.C., Austin C.C., Waddell P.J., Tibbets E.A.,	
RX			
Thomson N.R., James K.D., Harris D.E., Quail M.A., Challis G.R.,	RA	Ray J.N., Mindell D.P.;	
RA Bentley S.," Chater K.F., Cerdano-Tarraga A.-M., Kieser H.,	RA	"Molecular systematics of primary reptilian lineages and the tuatara	
RA Thomson D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,	RA	mitochondrial genome"; 0:0-0 (2003).	
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,	RA	EMBL: AF544390; MAP42708.1; -.	
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,	RA	Mitochondrion.	
RA Rabinowitch E., Rajandream M.A., Rutheford K., Rutter S.,	RA	SEQUENCE 228 AA; 25903 MW; AC52448F76C9F0A4 CRC64;	
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,	RA	Query Match 90.0%; Score 36; DB 8; Length 228;	
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,	RA	Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RA Hopwood D.A.;	RA	OY 2 DMSWA 6	
RT "Complete genome sequence of the model actinomycete Streptomyces	RT	Db 221 DMSWA 225	
RT coelicolor A3(2).";	RT		
RL Nature 417:141-147 (2002).	RL		
DR AL594464; CAC35779.1; -.	DR		
DR GO: GO-004821; C:extrachromosomal DNA; IBA.	DR		
KW Hypothetical protein; Plasmid; Complete Proteome.	KW		
SQ SEQUENCE 205 AA; 23051 MW; 6602396CFF93F2D9 CRC64;	SQ		
RESULT 12			
O8IXKB			
ID O8IXKB	PRELIMINARY;	PRT;	227 AA.
AC			
DT 01-MAR-2003 (TREMBrel. 23, Created)	ID	O919KB	PRELIMINARY;
DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)	AC	O919KB	PRELIMINARY;
DE Similar to hypothetical protein BC017335.	DT	01-DEC-2001 (TREMBrel. 19, Created)	
OS Homo sapiens (Human).	DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)	
OC Culex nigripalpus baculovirus.	DE	CUN068 hypothetical protein.	
OC Virus; dsDNA viruses, no RNA stage; Baculoviridae.	GN	CUN068 hypothetical protein.	
OX NCBI_TAXID=9606;	OC	Culex nigripalpus baculovirus.	
RN [1]	OC	Virus; dsDNA viruses, no RNA stage; Baculoviridae.	
RP	OX	NCBI_TAXID=13056;	
RC	RN	SEQUENCE FROM N.A.	
RC STRAIN=Florida997;	RC	SEQUENCE FROM N.A.	
RX MEDLINE=21488625; PubMed=11602755;	RX	AFONSO C.L., TULMAN E.R., BLINEVSKY C.A., MOSER B.A.,	
RA AFONSO C.L., TULMAN E.R., BLINEVSKY C.A., MOSER B.A.,	RA	BECKEL J.D., ROCK D.J., KUTTER G.F.,	
DE "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus."	RT	J. Virol. 75:11157-11165 (2001).	
OS Culex nigripalpus baculovirus.	RL	RT J. Virol. 75:11157-11165 (2001).	
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	RL		
OX NCBI_TAXID=9606;	RL		
RN [1]	RP	SEQUENCE FROM N.A.	

Query Match 90.0%; Score 36; DB 12; Length 242;
 Best Local Similarity 100.0%; Pred. No. 3 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy	2	DNSWA	6
	80	DNSWA	84

RBSLRT 15

Q8BIT9	PRELIMINARY;	PRT;	355 AA.
ID	Q8BIT9;		
AC			
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Mitochondrial ribosomal protein L41 homolog.		
GN	2810443J12Rik.		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI TaxID:10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NOD; TISSUE=Thymus;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	The RANTOM Consortium		
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."		
RT	Nature 420:563-573 (2002).		
DR	EMBL; AK087998; BAC40084.1; -.		
DR	MGI; MGI:1914478; 2810443J12Rik.		
DR	InterPro; IPR001680; WD40.		
DR	PFam; PF00000; WD40; 2.		
DR	SMART; SM00320; WD40; 4.		
DR	PROSITE; PS00678; WD_REPEATS_1; 1.		
DR	PROSITE; PS0294; WD_REPEATS_REGION; 1.		
SQ	SEQUENCE 355 AA; 40183 MW; PEF8546127402D58 CRC64;		

Query Match 90.0%; Score 36; DB 11; Length 355;
 Best Local Similarity 100.0%; Pred. No. 4 8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy	1	ANSW	5
	215	ADNSW	219

Search completed: April 26, 2004, 13:08:48
 Job time : 41 secs

Copyright (c) 1993 - 2004 CompuGen Ltd.									
GenCore version 5.1.6									
OM protein - protein search, using sw model									
Run on: April 26, 2004, 13:04:13 ; Search time 21 Seconds									
27.483 Million cell updates/sec									
Searched:	283366 seqs, 96191526 residues								
Total number of hits satisfying chosen parameters:	283366								
Minimum DB seq length:	0								
Maximum DB seq length:	200000000								
Post-processing:	Minimum Match 0%								
	Maximum Match 100%								
	Listing first 45 summaries								
Database :	PIR 78:*								
	1: pir1:*								
	2: pir2:*								
	3: pir3:*								
	4: pir4:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	% Query Match	Length	DB	ID	Description			
1	37	92.5	610	2	T35222	hypothetical protein sc5c7.15 sc5c7.15 - Streptomyces coelicolor	RESULT 1		
2	37	92.5	885	2	C83441	C-Species: Streptomyces coelicolor	T35222		
3	36	90.0	374	2	B83441	C-Accession: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999			
4	36	90.0	889	2	E87304	R-Accession: T35222			
5	34	85.0	275	2	T05022	R-Accession: K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.			
6	34	85.0	617	2	C84922	submitted to the EMBL Data Library, September 1998			
7	34	85.0	1842	2	T38781	A-Reference number: Z21572			
8	34	85.0	1842	2	T38781	A-Accession: T35222			
9	33	82.5	132	2	S65785	A-Status: preliminary; translated from GB/EMBL/DBJ			
10	33	82.5	198	2	B82531	A-Molecule type: DNA			
11	33	82.5	220	2	D64316	A-Residues: 1-610 <SEE>			
12	33	82.5	232	2	S58353	A-Cross-references: EMBL:AU031515; PIDN:CAA20527.1; GSPDB:GN000070; SC08DB:SC5C7.15			
13	33	82.5	239	2	D90470	A-Experimental source: strain A3(2)			
14	33	82.5	257	2	D87152	A-Gene: SC08DB:SC5C7.15			
15	33	82.5	276	2	B75337				
16	33	82.5	304	2	B83632	ALIGNMENTS			
17	33	82.5	310	2	JCT853	RESULT 2			
18	33	82.5	324	2	AB3548	Query Match 92.5%; Score 37; DB 2; Length 610;			
19	33	82.5	328	2	E74424	Best Local Similarity 83.3%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;			
20	33	82.5	333	2	S47246				
21	33	82.5	350	2	S71923	Query Match 92.5%; Score 37; DB 2; Length 885;			
22	33	82.5	368	2	H91998	Best Local Similarity 83.3%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;			
23	33	82.5	410	2	D75475				
24	33	82.5	415	2	AE1844	Query Match 92.5%; Score 37; DB 2; Length 885;			
25	33	82.5	418	2	AE1460	Best Local Similarity 83.3%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;			
26	33	82.5	418	2	AF01097				
27	33	82.5	421	2	T38422	Query Match 92.5%; Score 37; DB 2; Length 885;			
28	33	82.5	433	2	T31511	Best Local Similarity 83.3%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;			
29	33	82.5	467	2	G82897	Query Match 92.5%; Score 37; DB 2; Length 885;			
30	33	82.5	478	2	E89790	6-phospho-beta-glu			
31	33	82.5	499	2	139953	6-phospho-beta-glu			
32	33	82.5	499	2	S03098	aerolysin precursor			
33	33	82.5	529	2	C89958	probable GMP synth			
34	33	82.5	539	2	T12256	hypothetical prote			
35	33	82.5	578	2	C64452	restriction modifi			
36	33	82.5	590	2	S77813	GMP synthase (glut			
37	33	82.5	616	2	C65226	type I restriction			
38	33	82.5	623	2	E75222	type I restriction			
39	33	82.5	765	2	S75795	hypothetical prote			
40	33	82.5	836	2	D82177	conserved hypothet			
41	33	82.5	102	2	S71424	nitric-oxide synth			
42	33	82.5	103	1	A47501	nitric-oxide synth			
43	33	82.5	1205	1	A33943	conserved hypothet			
44	33	82.5	1229	2	D81226	alkaline phosphat			
45	33	82.5	1409	2	S77916	alkaline phosphat			

QY	1	ADMSWA 6	A;Accession: T05822
Db	563	ADWAWA 568	A;Molecule type: DNA
			A;Residues: 1-275
			A;Cross references: EMBL:AL022580
			A;Experimental source: cultivar Columbia; BAC clone TSK18
			C;Genetics:
			A;Map Position: 4
			A;Introns: 103/3/1 141/3; 169/1; 206/3
			A;Note: TSK18.170
			Query Match
			Best Local Similarity 85.0%; Score 34; DB 2; Length 275;
			Matches 4; Conservative 66.7%; Pred. No. 1.4e-02; 0; Mismatches 0; Indels 0; Gaps 0;
QY	2	DMSWA 6	A;Title: Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> .
Db	81	DMSWA 85	A;Reference number: A84420; MUID:20083487; PMID:10617197
			A;Accession: C84922
			A;Status: Preliminary
			A;Molecule type: DNA
			A;Residues: 1-617 <STO>
			A;Cross-references: GB:AE002093; NID:94249408; PIDN:AA013705.1; GSPDB:GN00139
			C;Genetics:
			A;Gene: At2g48010
			A;Map position: 2
			Query Match
			Best Local Similarity 85.0%; Score 34; DB 2; Length 617;
			Matches 4; Conservative 66.7%; Pred. No. 3.1e+02; 2; Mismatches 0; Indels 0; Gaps 0;
QY	1	ADMSWA 6	A;Title: Aberrant mitosis mutants defective in fatty acid synthetase and
Db	500	ADWAWA 505	A;Reference number: 222499; MUID:96354912; PMID:8769419
			A;Accession: T43409
			A;Status: Preliminary; translated from GB/EMBL/DDJB
			A;Molecule type: DNA
			A;Residues: 1-1842 <SA1>
			A;Cross-references: EMBL:D83412; NID:919959; PIDN:BA11913.1; PID:919960
			C;Genetics:
			A;Note: 1842
			C;Superfamily: yeast fatty-acid synthase
			C;Keywords: acyltransferase; coenzyme A
			Query Match
			Best Local Similarity 85.0%; Score 34; DB 2; Length 1842;
			Matches 4; Conservative 66.7%; Pred. No. 9.4e+02; 2; Mismatches 0; Indels 0; Gaps 0;
RESULT	5		A;Reference number: Z15453
T05822			A;Reference number: Z15453
			hypothetical protein T5K18.170 - <i>Arabidopsis thaliana</i> (mouse-ear cress)
			C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)
			C;Date: 23-Apr-1999 #Sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
			C;Accession: T05822
			R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voot, M.; Robben, J.; Volckaert, G.; Ba
			A;Reference number: 222499
			A;Reference number: Z15453

Qy 1 ADWSWA 6
Db 400 SDWNWA 405

RESULT 8

T38781 fatty acid synthase, subunit alpha - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Accession: T38781 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T38781 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: 221751
A;Accession: T38781 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-198 <SIM>
A;Cross-references: GB:AB004072; GB:AE003849; NID:9107884; PIDN:AAF85463.1; GSPDB:GN001;
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarezaga, R.; Al
Brioner, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; Bl-Dorcy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Perro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeri, D.A.
Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuchako, M.H.; Villada, H.; Van Sluys, M.A.; Verjovska-Almeida, S.; Vettore, A.L.; Ze
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gen: SPB:SPAC4A8.11c
A;Map position: 1
C;Superfamily: yeast fatty-acid synthase

Query Match Score 85.0%; Score 34; DB 2; Length 1842;

Best Local Similarity 66.7%; Pred. No. 9.4e+02; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 400 SDWNWA 405

RESULT 9

s65785 mel-13a protein - mouse

C;Species: *Mus musculus* (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999

C;Accession: S65785
R;Tetsu, O.; Kanno, R.; Isono, K.; Taniuchi, M.; Kanno, M.

Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene

A;Reference number: S65785; MUID:96180310; PMID:8597592

A;Accession: S65785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <TT>

A;Cross-references: EMBL:U35309
C;Genetics:
A;Gene: mel-13
C;Superfamily: mouse mel-13a protein
C;Keywords: alternative splicing

Query Match Score 82.5%; Score 33; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 9.6e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 57 SDWSW 61

RESULT 10

882531 conserved hypothetical protein XF2666 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C;Accession: B82531
R;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequer
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:1010347

A;Note: for a complete list of authors see reference number A59328 below

A;Accessions: B82531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <SIM>

A;Cross-references: GB:AB004072; GB:AE003849; NID:9107884; PIDN:AAF85463.1; GSPDB:GN001;

A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarezaga, R.; Al
Brioner, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; Bl-Dorcy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Perro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeri, D.A.
Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuchako, M.H.; Villada, H.; Van Sluys, M.A.; Verjovska-Almeida, S.; Vettore, A.L.; Ze
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gen: XFE666

C;Superfamily: conserved hypothetical protein MJ1677

Query Match Score 82.5%; Score 33; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 1.4e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
Db 135 DNWNWA 139

RESULT 11

D64316 restriction modification enzyme subunit M1 homolog - *Methanococcus jannaschii*

C;Species: *Methanococcus jannaschii*

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2002

C;Accession: D64316
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Suttorp, G.G.; Blake, J.;
Reich, C.I.; Overbeek, R.; Kirnness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*.
A;Reference number: D64316; MUID:933799; PMID:6688087

A;Accession: D64316
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-220 <BLU>
A;Cross-references: GB:U67470; GB:L77117; NID:92826247; PIDN:AAB98113.1; PID:91592267; T1

C;Genetics:
A;Map position: REV127472-126810
A;Start codon: TTT
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match Score 82.5%; Score 33; DB 2; Length 220;
Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 33 ADWA 37

RESULT 12

558333 CD1b protein - sheep (fragment)

C;Species: *Ovis orientalis aries*; *Ovis ammon aries* (domestic sheep)
C;Accession: S58333
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000

R;Ferguson, E.D.; Dutia, B.M.; Hein, W.; Hopkins, J.
A;Submitted to the EMBL Data Library, July 1995
C;Description: The ovine CD1 gene family contains at least four CD1B homologues.
A;Reference number: S58353
A;Accession: S58353
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <PER>
A;Cross-references: EMBL:X90567; NID:945010; PIDN:CAA62187_1; PID:945011
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;115-180/Domain: immunoglobulin homology <IM>
Query Match 82.5%; Score 33; DB 2; Length 232;
Best Local Similarity 80.0%; Pred. No. 1.7e+02; 0; Mismatches 4; Conservative 1; Indels 0; Gaps 0;
Matches 4; Mismatches 1;
Qy 1 ADWSW 5
Db 156 ADWTW 160

RESULT 13
D90470 hypothetical protein *cysH* [imported] - *Sulfolobus solfataricus*
C;Species: *Sulfolobus solfataricus*
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: D90470
R;She, O.; Singh, R.K.; Conflaloniri, F.; Zivanovic, Y.; Allard, G.; Awayerz, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Tri-Ngoc, H.P.; Redder, E.
arrett, R.A.; Ragan, M.A.; Simola, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: *Sulfolobus solfataricus* complete genome.
A;Reference number: A99139
A;Accession: A99139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-239 <KUR>
A;Cross-references: GB:AE006641; NID:g13181282; PIDN:AAK43019.1; GSPDB:GN00155
C;Genetics:
A;Gene: *CYSH*
C;Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase
Query Match 82.5%; Score 33; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 1.7e+02; Mismatches 4; Conservative 1; Indels 0; Gaps 0;
Matches 4; Mismatches 0;
Qy 1 ADWSW 5
Db 172 ADWTW 176

RESULT 14
D87152 conserved hypothetical protein *Mt1945* [imported] - *Mycobacterium leprae*
C;Species: *Mycobacterium leprae*
C;Accession: D87152 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-
eam, M.A.; Rutherford, K.M.
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
A;Accession: D87152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Cross-references: GB:AL450380; NID:g13093601; PIDN:CA30900.1; GSPDB:GN00147
C;Genetics:
A;Gene: *Mt1945*
C;Superfamily: *Mycobacterium tuberculosis* hypothetical protein *Rv1100*

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Query Match          82.5%;  Score 33;  DB 2;  Length 257;
Best Local Similarity 83.3%;  Pred. No. 1.9e+02;  1;  Indels 0;  Gaps 0;
Matches 5;  Conservative 0;  Mismatches 0;

QY          1 ADNSWA 6
Db          11 ATWSWA 16

RESULT 15
B75337
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: B75337
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shein, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75337
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <WHI>
A;Cross-references: GB:AE002032; GB:AE000513; NID:96459715; PIDN:AAF11479.1; PID:9645971
A;Experimental source: strain R1
A;Genetics:
A;Gene: DR1923
A;Map Position: 1

Query Match          82.5%;  Score 33;  DB 2;  Length 276;
Best Local Similarity 80.0%;  Pred. No. 2e+02;  1;  Indels 0;  Gaps 0;
Matches 4;  Conservative 1;  Mismatches 0;

QY          1 ADNSW 5
Db          84 ADWA 88

search completed: April 26, 2004, 13:09:21
Job time : 22 secs

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PT	CARBONYD	398	398	N-LINKED (GLCNAC. . .) (POTENTIAL).	Best Local Similarity 100.0%; Pred. No. 70; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ	SEQUENCE	470 AA;	51989 MW;	DIAGF07460F6FBAD CRC64;	
Query Match		90.0%;	Score 36;	DB 1;	Length 470;
Best Local Similarity	100.0%;	Pred. No.	70;		
Matches	5;	Conservative	0;	Mismatches	0;
QY	1	ADMSW 5			
Db	453	ADMSW 457			
RESULT 2					
NRAM_IADCH	STANDARD;	PRT;	470 AA.		
ID	NRAM_IADCH				
AC	Q07571;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Neuraminidase (EC 3.2.1.18).				
GN	NA.				
OS	Influenza A virus (strain A/Duck/Chabarovsk/1610/72)				
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;				
OC	Influenza A viruses; Influenzavirus A.				
OX	NCBI_TaxID:38957;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9312520; PubMed=8460490;				
RA	Saito T., Kawakita Y., Webster R.G.;				
RT	Phylogenetic analysis of the N8 neuraminidase gene of influenza A virus.				
RT	virology 133: 868-876(1993).				
RL	-.-. FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.				
CC	-.-. CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.				
CC	-.-. SUBUNIT: Homotetramer.				
CC	-.-. SUBUNIT: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.				
CC	-.-. SIMILARITY: Belongs to family 34 of glycosyl hydrolases.				
CC	-.-. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_licensee@isb-sib.ch).				
CC	-.-. EMBL; L06573; AAA43367.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	ProDom; PDD00431; Glyco_hydro_34.1.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
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DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	PFam; PF00064; neur. 1.				
DR	ProDom; PDD00431; Glyco_hydro_34.				
DR	EMBL; L06574; AAA43372.1; -.				
DR	HSSP; P06820; ZBART.				
DR	InterPro; IPR001860; Glyco_hydro_34				

RESULT 4		RESULT 5	
ID	NRAM_IADM3	ID	NRAM_IADM3
ID	NRAM_IADM2	STANDARD;	STANDARD;
AC	Q07573;	007599;	007599;
DT	01-FEB-1995 (Rel. 31, last sequence update)	01-OCT-1994 (Rel. 30, created)	01-OCT-1994 (Rel. 30, last sequence update)
DT	28-FEB-2003 (Rel. 41, last annotation update)	28-OCT-1994 (Rel. 30, last sequence update)	28-FEB-2003 (Rel. 41, last annotation update)
DE	Neuraminidase (EC 3.2.1.18).	Neuraminidase (EC 3.2.1.18).	Neuraminidase (EC 3.2.1.18).
GN	NA.	NA.	NA.
OS	Influenza A virus (strain A/Duck/Memphis/928/74).	Influenza A virus (strain A/Duck/Ukraine/1/63).	Influenza A virus (strain A/Duck/Ukraine/1/63).
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OX	NCBI_TaxID=11367;	NCBI_TaxID=11367;	NCBI_TaxID=11367;
RN	[1] SEQUENCE FROM N.A.	[1] SEQUENCE FROM N.A.	[1] SEQUENCE FROM N.A.
RP	Medline:93212520; PubMed=8460490;	Medline:93212520; PubMed=8460490;	Medline:93212520; PubMed=8460490;
RA	Saito T., Kawao Y., Webster R.G.;	Saito T., Kawao Y., Webster R.G.;	Saito T., Kawao Y., Webster R.G.;
RT	"Phylogenetic analysis of the NB neuraminidase gene of influenza A viruses.";	"Phylogenetic analysis of the NB neuraminidase gene of influenza A viruses.";	"Phylogenetic analysis of the NB neuraminidase gene of influenza A viruses.";
RL	Virology 193:868-876(1993).	Virology 193:868-876(1993).	Virology 193:868-876(1993).
CC	-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface protein and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.	-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface protein and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.	-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface protein and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
CC	-!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.	-!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.	-!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-!- SUBUNIT: Homotrimer.	-!- SUBUNIT: Homotrimer.	-!- SUBUNIT: Homotrimer.
CC	-!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.	-!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.	-!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
CC	-!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.	-!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.	-!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC	DR: EMBL; L06575; AAA43404.1; -.	DR: EMBL; L06576; AAA16234.1; -.	DR: EMBL; L06576; AAA16234.1; -.
CC	DR: HSSP; P06820; 2BAT.	DR: HSSP; P06820; 2BAT.	DR: HSSP; P06820; 2BAT.
CC	DR: InterPro; IPR01860; Glyco_hydro_34.	DR: InterPro; IPR01860; Glyco_hydro_34.	DR: InterPro; IPR01860; Glyco_hydro_34.
CC	DR: Pfam; PF00064; neur_1.	DR: Pfam; PF00064; neur_1.	DR: Pfam; PF00064; neur_1.
CC	DR: ProDom; PDD00431; Glyco_hydro_34.	DR: ProDom; PDD00431; Glyco_hydro_34.	DR: ProDom; PDD00431; Glyco_hydro_34.
CC	DR: KW: Hydrolase; Glycosidase; Glycoprotein; Transmembrane.	DR: KW: Hydrolase; Glycosidase; Glycoprotein; Transmembrane.	DR: KW: Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
CC	FT: TRANSMEM_7_38_ANCHOR (BY SIMILARITY).	FT: TRANSMEM_7_37_ANCHOR (BY SIMILARITY).	FT: TRANSMEM_7_37_ANCHOR (BY SIMILARITY).
CC	FT: DOMAIN_39_88_HEAD_NEURAMINIDASE.	FT: DOMAIN_38_88_HEAD_NEURAMINIDASE.	FT: DOMAIN_38_88_HEAD_NEURAMINIDASE.
CC	FT: ACT_SITE_273_273_BY_SIMILARITY.	FT: ACT_SITE_273_273_BY_SIMILARITY.	FT: ACT_SITE_273_273_BY_SIMILARITY.
CC	FT: ACT_SITE_275_275_BY_SIMILARITY.	FT: ACT_SITE_275_275_BY_SIMILARITY.	FT: ACT_SITE_275_275_BY_SIMILARITY.
CC	FT: DOMAIN_89_470_BY_SIMILARITY.	FT: DOMAIN_89_470_BY_SIMILARITY.	FT: DOMAIN_89_470_BY_SIMILARITY.
CC	FT: CARBOHYD_46_54_BY_SIMILARITY.	FT: CARBOHYD_46_54_BY_SIMILARITY.	FT: CARBOHYD_46_54_BY_SIMILARITY.
CC	FT: CARBOHYD_84_84_BY_SIMILARITY.	FT: CARBOHYD_84_84_BY_SIMILARITY.	FT: CARBOHYD_84_84_BY_SIMILARITY.
CC	FT: ACT_SITE_275_275_BY_SIMILARITY.	FT: ACT_SITE_275_275_BY_SIMILARITY.	FT: ACT_SITE_275_275_BY_SIMILARITY.
CC	FT: DOMAIN_45_45_BY_SIMILARITY.	FT: DOMAIN_45_45_BY_SIMILARITY.	FT: DOMAIN_45_45_BY_SIMILARITY.
CC	FT: CARBOHYD_54_54_BY_SIMILARITY.	FT: CARBOHYD_54_54_BY_SIMILARITY.	FT: CARBOHYD_54_54_BY_SIMILARITY.
CC	FT: CARBOHYD_144_144_BY_SIMILARITY.	FT: CARBOHYD_144_144_BY_SIMILARITY.	FT: CARBOHYD_144_144_BY_SIMILARITY.
CC	FT: CARBOHYD_398_398_BY_SIMILARITY.	FT: CARBOHYD_398_398_BY_SIMILARITY.	FT: CARBOHYD_398_398_BY_SIMILARITY.
CC	FT: SEQUENCE_470_AA_51960_MW_BY_SIMILARITY.	FT: SEQUENCE_470_AA_51960_MW_BY_SIMILARITY.	FT: SEQUENCE_470_AA_51960_MW_BY_SIMILARITY.
CC	Query Match 90.0%; score 36; DB 1; Length 470; Best Local Similarity 100.0%; Pred. No. 70; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 90.0%; score 36; DB 1; Length 470; Best Local Similarity 100.0%; Pred. No. 70; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 90.0%; score 36; DB 1; Length 470; Best Local Similarity 100.0%; Pred. No. 70; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	SQ: SEQUENCE_470_AA_51960_MW_BY_SIMILARITY.	SQ: SEQUENCE_470_AA_51960_MW_BY_SIMILARITY.	SQ: SEQUENCE_470_AA_51960_MW_BY_SIMILARITY.

chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3), alpha-(2->6), alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

-!- SUBUNIT: Homotetramer. Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.

-!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

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CC EMBL; L06588; AA043410.1; -.

CC HSSP; P06820; 2BKT.

CC DR InterPro; IPR001860; Glyco_hydro_34.

CC DR Pfam; PF0064; neur; 1.

CC DR Prodom; PDD00431; Glyco_hydro_34; 1.

CC KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

CC FT TRANSMEM; 7; 38; ANCHOR (BY SIMILARITY).

CC FT DOMAIN; 39; 88; HYPERVARIABLE STALK REGION.

CC FT ACT_SITE; 273; 273; BY SIMILARITY.

CC FT ACT_SITE; 275; 275; BY SIMILARITY.

CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 46; 54; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 54; 84; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 144; 144; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 293; 398; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 398; 398; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SQ SEQUENCE; 470 AA; 52352 MW; DE573742BFRF16B CRC64;

CC Query Match 90.0%; Score 36; DB 1; Length 470;

CC Best Local Similarity 100.0%; Pred. No. 70; Mismatches 0; Indels 0; Gaps 0;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Ov 1 ADNSW 5

CC Db 453 ADNSW 457

RESULT 11
MRJ5_APIME STANDARD; PRT; 598 AA.

AC 097432;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).

GN MRJPs.

OS Apis mellifera (Honeybee).

OC Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Acoidea;

OC Apidae; Apis.

OX NCBI_TaxID:7460;

RN [1]

RP SOURCE FROM N.A.

RC TISSUE=Head;

CC "The family of major royal jelly proteins and its evolution." J. Mol. Evol. 49:290-297(1999).

-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE

HONEYBEE QUEEN.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.

-!- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of the nurse honey bee.

-!- SIMILARITY: Belongs to the major royal jelly protein family.

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CC EMBL; AF00842; AAD01205.1; -.

CC DR InterPro; IPR003534; Royaljelly.

CC DR Pfam; PF03022; MRJ5; 2.

CC DR PRINTS; PRO1366; ROYALJELLY.

CC KW SIGNAL; Repeat; Glycoprotein.

CC FT SIGNAL; Repeat; 1; 17; POTENTIAL.

CC FT CHAIN; 18; 598; MAJOR ROYAL JELLY PROTEIN 5.

CC FT CARBOHYD; 148; 148; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 164; 164; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 181; 181; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD; 324; 324; N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SQ 598 AA; 70236 MW; 2C603C77E/FACDF63 CRC64;

CC Query Match 90.0%; Score 36; DB 1; Length 598;

CC Best Local Similarity 100.0%; Pred. No. 87;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Ov 2 DMSWA 6

CC Db 113 DMSWA 117

RESULT 12
PGLR_PENGR STANDARD; PRT; 376 AA.

AC 093865;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Polygalacturonase precursor (EC 3.2.1.15) (PGI) (Pectinase).

GN PGI.

OS penicillium griseoeseum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiidae; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

OX NCBI_TaxID:84562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRATN-CC7 6421;

Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;

RR "Cloning and characterization of a gene encoding the endopolygalacturonase of *Penicillium griseoeseum*."

RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronate linkages in pectate and other galacturonans.

CC -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_licensee@isb-sib.ch).

CC EMBL; AF08328; AAC03692.1; -.

CC DR InterPro; IPR00743; Glyco_hydro_28.

CC DR InterPro; IPR006626; PDB1.

CC DR Pfam; PF0295; Glyco_hydro_28; 1.

SQ	SEQUENCE	1842 AA;	202168 MW;	E4019F20133EE571 CRC64;
Query Match	85.0%	Score 34;	DB 1;	Length 1842;
Best Local Similarity	66.7%	Pred. No. 4	9e+02;	
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Qy	1	AMWSWA 6	400	SDWNWA 405
Db				
RESULT 14				
NOS3_SHEEP				
ID -NOS3_SHEEP		STANDARD;		
AC P79209;		PRT;	99 AA.	
DT 30-MAY-2000 (Rel. 39, Created)				
DT 30-MAY-2000 (Rel. 39, Last sequence update)				
DT 30-MAY-2000 (Rel. 39, Last annotation update)				
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (Constitutive NOS) (cNOS) (Fragment)				
DE (Fragment)				
GN NOS3 OR ENOS				
OS Ovis aries (Sheep).				
OC Bovkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; OC Bovidae; Caprinae; Ovis.				
OC NCBI_TaxID:9940;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE:Endothelial cells;				
RA Aquan K., Weiner C.P.;				
RT "Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase.";				
RT Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.				
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. No mediates vascular endothelial growth factor (VEGFR)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets (By similarity).				
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).				
CC -!- COPACTOR: Heme. Binds one mole each of FAD and FMN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).				
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin (By similarity).				
CC -!- SUBUNIT: Homodimer (By similarity).				
CC -!- SIMILARITY: Belongs to the NOS family.				
CC				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use. By non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).				
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DR PIR; D64316; D64316.				
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DR Pfam; PF02888; NO_synthase_1.				
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Mon Apr 26 14:30:00 2004

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 26, 2004, 13:06:38 ; Search time 23 Seconds
(without alignments)
13.468 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*

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5: /cgn2_6/ptodata/2/iaa/PCRS_Comb.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	37	92.5	236	4	US-09-632-570-17
2	37	92.5	236	4	US-09-632-570-17
3	37	92.5	938	4	US-09-252-991A-23082
4	36	90.0	68	4	US-09-232-991A-18367
5	36	90.0	142	4	US-09-232-991A-31533
6	36	90.0	174	4	US-09-325-932A-163
7	36	90.0	225	4	US-09-325-932A-162
8	36	90.0	242	4	US-09-325-932B-3
9	36	90.0	378	4	US-09-325-932A-158
10	36	90.0	445	4	US-09-252-991A-22368
11	36	90.0	462	4	US-09-232-991A-21704
12	34	85.0	44	3	US-08-905-223-274
13	33	82.5	74	1	US-08-319-538-2
14	33	82.5	136	2	US-08-774-565-2
15	33	82.5	164	4	US-09-252-991A-23817
16	33	82.5	218	1	US-08-032-840C-10
17	33	82.5	218	1	US-08-438-870-10
18	33	82.5	218	2	US-08-159-940B-34
19	33	82.5	218	2	US-08-438-873-34
20	33	82.5	218	3	US-08-382-452D-34
21	33	82.5	218	3	US-09-216-295-1
22	33	82.5	218	4	US-08-307-362A-18
23	33	82.5	218	4	US-09-916-490A-34
24	33	82.5	218	4	US-09-632-570-1
25	33	82.5	218	4	US-09-632-575-31
26	33	82.5	232	3	US-09-140-770-1
27	33	82.5	232	4	US-09-633-084-1

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
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4	83.5	47	236	4	Sequence 17, Appl
5	83.5	47	236	4	Sequence 17, Appl
6	83.5	47	236	4	Sequence 17, Appl
7	83.5	47	236	4	Sequence 17, Appl
8	83.5	47	236	4	Sequence 17, Appl
9	83.5	47	236	4	Sequence 17, Appl
10	83.5	47	236	4	Sequence 17, Appl
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22	83.5	47	236	4	Sequence 17, Appl
23	83.5	47	236	4	Sequence 17, Appl
24	83.5	47	236	4	Sequence 17, Appl
25	83.5	47	236	4	Sequence 17, Appl
26	83.5	47	236	4	Sequence 17, Appl
27	83.5	47	236	4	Sequence 17, Appl

SEQUENCES

Result No.	Score	Query Match	Length	DB ID	Description
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3	83.5	47	236	4	Sequence 17, Appl
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5	83.5	47	236	4	Sequence 17, Appl
6	83.5	47	236	4	Sequence 17, Appl
7	83.5	47	236	4	Sequence 17, Appl
8	83.5	47	236	4	Sequence 17, Appl
9	83.5	47	236	4	Sequence 17, Appl
10	83.5	47	236	4	Sequence 17, Appl
11	83.5	47	236	4	Sequence 17, Appl
12	83.5	47	236	4	Sequence 17, Appl
13	83.5	47	236	4	Sequence 17, Appl
14	83.5	47	236	4	Sequence 17, Appl
15	83.5	47	236	4	Sequence 17, Appl
16	83.5	47	236	4	Sequence 17, Appl
17	83.5	47	236	4	Sequence 17, Appl
18	83.5	47	236	4	Sequence 17, Appl
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20	83.5	47	236	4	Sequence 17, Appl
21	83.5	47	236	4	Sequence 17, Appl
22	83.5	47	236	4	Sequence 17, Appl
23	83.5	47	236	4	Sequence 17, Appl
24	83.5	47	236	4	Sequence 17, Appl
25	83.5	47	236	4	Sequence 17, Appl
26	83.5	47	236	4	Sequence 17, Appl
27	83.5	47	236	4	Sequence 17, Appl

Query Match 92.5%; Score 37; DB 4; Length 236;
 Best Local Similarity 83.3%; Pred. No. 89;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
 Db 63 ADMSWS 68

RESULT 3
 US-09-252-991A-23882
 Sequence 23882, Application US/09252991A
 Patent No. 6531795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenstein et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074, 788
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 23882
 LENGTH: 93
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-23882

Query Match 92.5%; Score 37; DB 4; Length 938;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
 Db 581 ADMSWA 586

RESULT 4
 US-09-252-991A-18367
 Sequence 18367, Application US/09252991A
 Patent No. 6531795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenstein et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074, 788
 PRIOR FILING DATE: 1998-02-18
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 18367
 LENGTH: 68
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18367

Query Match 90.0%; Score 36; DB 4; Length 68;
 Best Local Similarity 100.0%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
 Db 2 DMSWA 6

RESULT 5

Query Match 90.0%; Score 36; DB 4; Length 68;
 Best Local Similarity 100.0%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
 Db 2 DMSWA 6

RESULT 6
 US-09-325-932A-163
 Sequence 163, Application US/09325932A
 Patent No. 6451604
 GENERAL INFORMATION:
 APPLICANT: Flinn, Barry
 TITLE OF INVENTION: Compositions affecting programmed cell death and their use in the modification of forestry plant developer
 FILE REFERENCE: 10122
 CURRENT APPLICATION NUMBER: US/09/325, 932A
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 206
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 163
 LENGTH: 174
 TYPE: PRT
 ORGANISM: Eucalyptus grandis
 US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;
 Best Local Similarity 100.0%; Pred. No. 93; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
 Db 109 ADMSW 113

RESULT 7
 US-09-325-932A-162
 Sequence 162, Application US/09325932A
 Patent No. 6451604
 GENERAL INFORMATION:
 APPLICANT: Flinn, Barry
 TITLE OF INVENTION: Compositions affecting programmed cell death and their use in the modification of forestry plant developer
 FILE REFERENCE: 10122
 CURRENT APPLICATION NUMBER: US/09/325, 932A
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 206
 SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
; US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSN 5
Db 100 ADWSN 104

RESULT 8
US-09-345-236B-3
; Sequence 3, Application US/09345236B
; Patent No. 652154
; GENERAL INFORMATION:
; APPLICANT: Bechtel, James J.
; APPLICANT: Tukio, Fukuda
; APPLICANT: Moser, Bettina
; APPLICANT: Cochburn, Andrew
; APPLICANT: White, Susan E.
; APPLICANT: Underen, Albert H.
; TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal Compositions, and Methods for Control of Invertebrates
; FILE REFERENCE: 21042.0004
; CURRENT APPLICATION NUMBER: US/09/345,236B
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 242
; TYPE: PRT
; ORGANISM: mosquito baculovirus
; US-09-345-236B-3

Query Match 90.0%; Score 36; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 80 DWSWA 84

RESULT 9
US-09-325-932A-158
; Sequence 158, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flint, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell death and their use in the modification of forestry plant develo
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
; US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSN 5
Db 100 ADWSN 104

RESULT 10
US-09-252-991A-2236B
; Sequence 2236B, Application US/09252991A
; Patent No. 655195
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIORITY NUMBER: US 60/094,190
; PRIORITY FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2236B
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-2236B

Query Match 90.0%; Score 36; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 304 DWSWA 308

RESULT 11
US-09-252-991A-21704
; Sequence 21704, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIORITY NUMBER: US 60/074,788
; PRIORITY FILING DATE: 1998-02-18
; PRIORITY APPLICATION NUMBER: US 60/094,190
; PRIORITY FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21704
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 169 DWSWA 173

RESULT 12
US-08-905-223-274
; Sequence 274, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duleit, Aymeric
; US-08-905-223-274

```

APPLICANT: Lacroix, Bruno
 TITLE OF INVENTION: 5, ESTs FOR SECRETED PROTEINS
 NUMBER OF SEQUENCES: 503
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 501 West Broadway
 CITY: San Diego
 STATE: California
 ZIP: 92101-3505
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Win95
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/379,538
 FILING DATE: 3-MAY-1995
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelien, Ned A.
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 274:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 44 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 ORIGINAL SOURCE:
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: -26..1
 IDENTIFICATION METHOD: Von Heijne matrix
 OTHER INFORMATION: score 9.6
 OTHER INFORMATION: seq WLIALASWSWALC/RI
 US-08-905-233-274

Query Match 85.0%; Score 34; DB 3; Length 44;
 Best Local Similarity 83.3%; Pred. No. 48; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 1; Gaps 0;
 Qy 1 ADMSWA 6
 Db 19 ASHMSWA 24

RESULT 13
 US-08-379-538-2
 Sequence 2, Application US/08379538
 Patent No. 5804554
 GENERAL INFORMATION:
 APPLICANT: Volkmann, Robert A.
 APPLICANT: Saccocciano, Nicholas A.
 APPLICANT: Nason II, Deane M.
 APPLICANT: Heck, Steven D.
 APPLICANT: Ronau, Robert T.
 TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
 TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pfizer Inc
 STREET: 235 East 42nd Street
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10017
 COMPUTER READABLE FORM:
 CLASSIFICATION: 516
 ATTORNEY/AGENT INFORMATION:
 NAME: Zieliński, Bryan
 REGISTRATION NUMBER: 34,462
 REFERENCE/DOCKET NUMBER: PCT/US93/03921
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 573-4585
 TELEFAX: (212) 573-1939
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 74 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 LENGTH: 74 amino acids
 ANTI-SENSE: No
 ORIGINAL SOURCE:
 ORGANISM: Filistata hibernalis
 TISSUE TYPE: venom
 US-08-379-538-2

RESULT 14
 US-08-774-065-2
 Sequence 2, Application US/08774065
 Patent No. 5889899
 GENERAL INFORMATION:
 APPLICANT: Bower, Benjamin
 APPLICANT: Clarkson, Kathleen
 APPLICANT: Larens, Edmund
 APPLICANT: Ward, Michael
 APPLICANT: Clark, Michael
 APPLICANT: Ward, Michael
 TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS AND
 TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: GENENCOR INTERNATIONAL
 STREET: 925 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Discrete
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEE FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/774,065
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaister, Debra J.
 REGISTRATION NUMBER: 33, 889
 REFERENCE/DOCKET NUMBER: GC:68
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-6504
 TELEFAX: 415-845-6504
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 136 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-774-065-2

Query Match 82.5%; Score 33; DB 2; Length 136;
 Best Local Similarity 66.7%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0;
 Gaps 0;
 Qy 1 ADWSWA 6
 Db 62 ADWQWS 67

RESULT 15

US-09-252-991A-23817

; Sequence 23817, Application US/09252991A

; Parent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfeld et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107195_136

; CURRENT APPLICATION NUMBER: US/09/252, 991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074, 788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094, 190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 23817

; LENGTH: 164

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

; US-09-252-991A-23817

Query Match 82.5%; Score 33; DB 4; Length 164;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;
 Qy 1 ADWSWA 6
 Db 132 AGWSWA 137

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 Job time : 24 secs

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OM protein - protein search, using sw model
Run on: April 26, 2004, 13:07:38 ; Search time 181 Seconds
(without alignments)
32.355 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues
Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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RESULT	Query	Match Length	DB ID	Description
1	US-09-847-940C-6.rapm	6	US-09-847-940B-4	Sequence 6, Appli
2	US-09-847-940C-6.rapm	6	US-09-847-940A-41	Sequence 41, Appli
3	US-09-847-940C-6.rapm	6	US-09-847-946A-73	Sequence 73, Appli
4	US-09-847-940C-6.rapm	7	US-09-847-946A-77	Sequence 77, Appli
5	US-09-847-940C-6.rapm	8	US-09-847-946A-70	Sequence 70, Appli
6	US-09-847-940C-6.rapm	8	US-09-847-946A-78	Sequence 78, Appli
7	US-09-847-940C-6.rapm	9	US-09-847-946A-69	Sequence 69, Appli
8	US-09-847-940C-6.rapm	9	US-09-847-946A-72	Sequence 72, Appli
9	US-09-847-940C-6.rapm	9	US-09-847-946A-75	Sequence 75, Appli
10	US-09-847-940C-6.rapm	9	US-09-847-946A-76	Sequence 76, Appli
11	US-09-847-940C-6.rapm	10	US-09-847-946A-71	Sequence 71, Appli
12	US-09-847-940C-6.rapm	10	US-09-847-946A-74	Sequence 74, Appli
13	US-09-847-940C-6.rapm	11	US-09-847-946A-68	Sequence 68, Appli
14	US-09-847-940C-6.rapm	11	US-09-847-946A-549	Sequence 1549, Appli
15	US-09-847-940C-6.rapm	13	US-09-847-946A-45	Sequence 45, Appli
16	US-09-847-940C-6.rapm	15	US-09-847-946A-47	Sequence 47, Appli
17	US-09-847-940C-6.rapm	15	US-09-847-946A-17	Sequence 17, Appli
18	US-09-847-940C-6.rapm	16	US-09-847-946A-22	Sequence 16, Appli
19	US-09-847-940C-6.rapm	16	US-09-847-946A-22	Sequence 16, Appli
20	US-09-847-940C-6.rapm	18	US-09-847-946A-47	Sequence 18, Appli
21	US-09-847-940C-6.rapm	20	US-09-847-946A-17	Sequence 20, Appli
22	US-09-847-940C-6.rapm	20	US-09-847-946A-17	Sequence 20, Appli
23	US-09-847-940C-6.rapm	23	US-09-847-946A-17	Sequence 23, Appli
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35	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
36	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
37	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
38	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
39	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
40	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
41	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
42	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
43	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
44	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli
45	US-09-847-940C-6.rapm	24	US-09-847-946A-17	Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-09-643-260-6
US-09-643-260-6
; Sequence 6, Application US/09643260
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; INVENTOR: Ghosh, Sanjari
; TITLE OF INVENTION: Inhibition of NF-kappa B Activation by Blockade of IKK
; TITLE OF INVENTION: bea-NEMO Interactions at the NEMO Binding Domain
; FILE REFERENCE: 44574-5066-US
; CURRENT APPLICATION NUMBER: US/09/643-260
; CURRENT FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/253,288
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutant
; OTHER INFORMATION: peptide sequence
US-09-643-260-6

Query Match	Score 40;	DB 20;	Length 6;	US-09-847-946A-73
Best Local Similarity	100.0%;	Pred. No. 5.5e+06;	Mismatches 0;	Matches 6;
Matches	6;	Conservative 0;	Indels 0;	Gaps 0;
1 ADWSWA 6				
b 1 ADWSWA 6				
RESULT 2				
S-09-847-946A-41	Sequence 41, Application US/09847946A	Score 40;	DB 20;	Length 6;
GENERAL INFORMATION:	Sequence 77, Application US/09847946A	100.0%;	Score 40;	DB 23;
APPLICANT: May, Michael J	GENERAL INFORMATION:	Best Local Similarity	Length 6;	
APPLICANT: Ghosh, Sankar	APPLICANT: May, Michael J	100.0%;	Pred. No. 5.5e+06;	Mismatches 0;
APPLICANT: Findels, Mark A	APPLICANT: Ghosh, Sankar	0;	Conservative 0;	Indels 0;
APPLICANT: Phillips, Kathryn	APPLICANT: Findels, Mark A	0;	Indels 0;	Gaps 0;
APPLICANT: Hanning, Gerhard	APPLICANT: Phillips, Kathryn	0;	Indels 0;	
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF	TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF	0;	Indels 0;	
FILE REFERENCE: PPI-119	FILE REFERENCE: PPI-119	0;	Indels 0;	
CURRENT APPLICATION NUMBER: US/09/847, 946A	CURRENT APPLICATION NUMBER: US/09/847, 946A	0;	Indels 0;	
CURRENT FILING DATE: 2001-05-02	CURRENT FILING DATE: 2001-05-02	0;	Indels 0;	
PRIOR APPLICATION NUMBER: 60/201, 261	PRIOR APPLICATION NUMBER: 60/201, 261	0;	Indels 0;	
PRIOR FILING DATE: 2000-05-02	PRIOR FILING DATE: 2000-05-02	0;	Indels 0;	
PRIOR APPLICATION NUMBER: 09/643, 260	PRIOR APPLICATION NUMBER: 09/643, 260	0;	Indels 0;	
PRIOR FILING DATE: 2000-08-22	PRIOR FILING DATE: 2000-08-22	0;	Indels 0;	
NUMBER OF SEQ ID NOS: 160	NUMBER OF SEQ ID NOS: 160	0;	Indels 0;	
SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: PatentIn Ver. 2.0	0;	Indels 0;	
SEQ ID NO 41	SEQ ID NO 77	0;	Indels 0;	
LENGTH: 6	LENGTH: 7	0;	Indels 0;	
TYPE: PRT	TYPE: PRT	0;	Indels 0;	
ORGANISM: Artificial Sequence	ORGANISM: Artificial Sequence	0;	Indels 0;	
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding	FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding	0;	Indels 0;	
OTHER INFORMATION: sequence	OTHER INFORMATION: sequence	0;	Indels 0;	
S-09-847-946A-41	S-09-847-946A-77	0;	Indels 0;	
RESULT 4				
US-09-847-946A-77	Sequence 77, Application US/09847946A	100.0%;	Score 40;	DB 23;
GENERAL INFORMATION:	Sequence 77, Application US/09847946A	Best Local Similarity	Length 6;	
APPLICANT: May, Michael J	GENERAL INFORMATION:	100.0%;	Pred. No. 5.5e+06;	Mismatches 0;
APPLICANT: Ghosh, Sankar	APPLICANT: May, Michael J	0;	Conservative 0;	Indels 0;
APPLICANT: Findels, Mark A	APPLICANT: Ghosh, Sankar	0;	Indels 0;	Gaps 0;
APPLICANT: Phillips, Kathryn	APPLICANT: Findels, Mark A	0;	Indels 0;	
APPLICANT: Hanning, Gerhard	APPLICANT: Phillips, Kathryn	0;	Indels 0;	
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF	TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF	0;	Indels 0;	
FILE REFERENCE: PPI-119	FILE REFERENCE: PPI-119	0;	Indels 0;	
CURRENT APPLICATION NUMBER: US/09/847, 946A	CURRENT APPLICATION NUMBER: US/09/847, 946A	0;	Indels 0;	
CURRENT FILING DATE: 2001-05-02	CURRENT FILING DATE: 2001-05-02	0;	Indels 0;	
PRIOR APPLICATION NUMBER: 60/201, 261	PRIOR APPLICATION NUMBER: 60/201, 261	0;	Indels 0;	
PRIOR FILING DATE: 2000-05-02	PRIOR FILING DATE: 2000-05-02	0;	Indels 0;	
PRIOR APPLICATION NUMBER: 09/643, 260	PRIOR APPLICATION NUMBER: 09/643, 260	0;	Indels 0;	
PRIOR FILING DATE: 2000-08-22	PRIOR FILING DATE: 2000-08-22	0;	Indels 0;	
NUMBER OF SEQ ID NOS: 160	NUMBER OF SEQ ID NOS: 160	0;	Indels 0;	
SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: PatentIn Ver. 2.0	0;	Indels 0;	
SEQ ID NO 41	SEQ ID NO 77	0;	Indels 0;	
LENGTH: 6	LENGTH: 7	0;	Indels 0;	
TYPE: PRT	TYPE: PRT	0;	Indels 0;	
ORGANISM: Artificial Sequence	ORGANISM: Artificial Sequence	0;	Indels 0;	
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding	FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding	0;	Indels 0;	
OTHER INFORMATION: sequence	OTHER INFORMATION: sequence	0;	Indels 0;	
S-09-847-946A-73	S-09-847-946A-77	0;	Indels 0;	
RESULT 5				
US-09-847-946A-70	Sequence 70, Application US/09847946A	100.0%;	Score 40;	DB 23;
GENERAL INFORMATION:	Sequence 70, Application US/09847946A	Best Local Similarity	Length 7;	
APPLICANT: May, Michael J	GENERAL INFORMATION:	100.0%;	Pred. No. 5.5e+06;	Mismatches 0;
APPLICANT: Ghosh, Sankar	APPLICANT: May, Michael J	0;	Conservative 0;	Indels 0;
APPLICANT: Findels, Mark A	APPLICANT: Ghosh, Sankar	0;	Indels 0;	Gaps 0;
APPLICANT: Phillips, Kathryn	APPLICANT: Findels, Mark A	0;	Indels 0;	
APPLICANT: Hanning, Gerhard	APPLICANT: Phillips, Kathryn	0;	Indels 0;	
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF	TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF	0;	Indels 0;	
FILE REFERENCE: PPI-119	FILE REFERENCE: PPI-119	0;	Indels 0;	
CURRENT APPLICATION NUMBER: US/09/847, 946A	CURRENT APPLICATION NUMBER: US/09/847, 946A	0;	Indels 0;	
CURRENT FILING DATE: 2001-05-02	CURRENT FILING DATE: 2001-05-02	0;	Indels 0;	
PRIOR APPLICATION NUMBER: 60/201, 261	PRIOR APPLICATION NUMBER: 60/201, 261	0;	Indels 0;	
PRIOR FILING DATE: 2000-05-02	PRIOR FILING DATE: 2000-05-02	0;	Indels 0;	
PRIOR APPLICATION NUMBER: 09/643, 260	PRIOR APPLICATION NUMBER: 09/643, 260	0;	Indels 0;	
PRIOR FILING DATE: 2000-08-22	PRIOR FILING DATE: 2000-08-22	0;	Indels 0;	
NUMBER OF SEQ ID NOS: 160	NUMBER OF SEQ ID NOS: 160	0;	Indels 0;	
SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: PatentIn Ver. 2.0	0;	Indels 0;	
SEQ ID NO 73	SEQ ID NO 70	0;	Indels 0;	
LENGTH: 6	LENGTH: 8	0;	Indels 0;	
TYPE: PRT	TYPE: PRT	0;	Indels 0;	
ORGANISM: Artificial Sequence	ORGANISM: Artificial Sequence	0;	Indels 0;	
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding	FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding	0;	Indels 0;	
OTHER INFORMATION: sequence	OTHER INFORMATION: sequence	0;	Indels 0;	

; OTHER INFORMATION: sequence
; US-09-847-946A-70

Query Match 100.0%; Score 40; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 6; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 3 ADWSWA 8

RESULT 6
US-09-847-946A-78

; Sequence 78, Application US/09847946A
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643, 260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
; US-09-847-946A-78

Query Match 100.0%; Score 40; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 6; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 7
US-09-847-946A-69

; Sequence 69, Application US/09847946A
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643, 260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
; US-09-847-946A-69

Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 6; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 8
US-09-847-946A-72

; Sequence 72, Application US/09847946A
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643, 260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
; US-09-847-946A-72

Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 6; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 9
US-09-847-946A-75

; Sequence 75, Application US/09847946A
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hanning, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR APPLICATION NUMBER: 60/201, 261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643, 260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
; US-09-847-946A-75

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

Query Match Best Local Similarity 100.0%; Score 40; DB 23; Length 9; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gap 0

Qy	1 ADWSWA 6	2 ADWSWA 7	3 ADWSWA 8	Db
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RESULT 10

US-09-847-946A-76

; Sequence 76, Application US/09847946A

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Fineis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Haning, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847.946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 76

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

US-09-847-946A-76

Query Match Best Local Similarity 100.0%; Score 40; DB 23; Length 9; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gap 0

Qy	1 ADWSWA 6	2 ADWSWA 7	Db
----	------------	------------	----

RESULT 11

US-09-847-946A-71

; Sequence 71, Application US/09847946A

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Fineis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Haning, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847.946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 71

; LENGTH: 10

; TYPE: PRT

Qy	1	ADNSWA 6	100.0%; Score 40; DB 23; Length 10; Best Local Similarity 100.0%; Pred. No. 90; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OTHER INFORMATION: sequence
Db	2	ADNSWA 7	
RESULT 12			
US-09-847-946A-74			
; Sequence 74 Application US/09847946A			
; GENERAL INFORMATION:			
; APPLICANT: May, Michael J			
; APPLICANT: Ghosh, Sankar			
; APPLICANT: Fineis, Mark A			
; APPLICANT: Phillips, Kathryn			
; APPLICANT: Hanning, Gerhard			
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF			
; FILE REFERENCE: PPI-119			
; CURRENT APPLICATION NUMBER: US/09/847, 946A			
; CURRENT FILING DATE: 2001-05-02			
; PRIOR APPLICATION NUMBER: 60/201, 261			
; PRIOR FILING DATE: 2000-05-02			
; PRIOR APPLICATION NUMBER: 09/543, 260			
; PRIOR FILING DATE: 2000-08-22			
; NUMBER OF SEQ ID NOS: 160			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 74			
; LENGTH: 10			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial sequence: NEMO binding			
; OTHER INFORMATION: sequence			
US-09-847-946A-74			
Query Match			
Best Local Similarity		100.0%	
Matches		6;	
Db	3	ADNSWA 8	Score 40; DB 23; Length 10; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
RESULT 13			
US-09-847-946A-68			
; Sequence 68 Application US/09847946A			
; GENERAL INFORMATION:			
; APPLICANT: May, Michael J			
; APPLICANT: Ghosh, Sankar			
; APPLICANT: Fineis, Mark A			
; APPLICANT: Phillips, Kathryn			
; APPLICANT: Hanning, Gerhard			
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF			
; FILE REFERENCE: PPI-119			
; CURRENT APPLICATION NUMBER: US/09/847, 946A			
; CURRENT FILING DATE: 2001-05-02			
; PRIOR APPLICATION NUMBER: 60/201, 261			
; PRIOR FILING DATE: 2000-05-02			
; PRIOR APPLICATION NUMBER: 09/543, 260			
; PRIOR FILING DATE: 2000-08-22			
; NUMBER OF SEQ ID NOS: 160			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 68			
LENGTH: 11			

TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
us-09-847-940c-6

Query Match 100.0%; Score 40; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 97; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 3 ADWSWA 8

RESULT 14
PCT-US01-01321-1549

Sequence 1549, Application PC/TUS0101321

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc., et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC011PCT

CURRENT APPLICATION NUMBER: PCT/US01/01321

CURRENT FILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 2181

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1549

LENGTH: 33

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

LOCATION: (3)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

PCT-US01-01321-1549

Query Match 92.5%; Score 37; DB 1; Length 33;

Best Local Similarity 83.3%; Pred. No. 6e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 9 ADWTWA 14

RESULT 15
US-09-284-327A-45

Sequence 45, Application US/09284327A

GENERAL INFORMATION:

APPLICANT: Bower, Benjamin S.

APPLICANT: Fowler, Timothy

APPLICANT: Phillips, Jay T.

TITLE OF INVENTION: Novel EGIII-Like Enzymes, DNA Encoding

FILE REFERENCE: G516-2-US

CURRENT APPLICATION NUMBER: US/09/284,327A

CURRENT FILING DATE: 1999-04-10

PRIOR APPLICATION NUMBER: PCT/US98/26552

PRIOR FILING DATE: 1998-12-14

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 45

LENGTH: 103

TYPE: PRT

ORGANISM: Giocladium roseum

US-09-284-327A-45

Query Match 92.5%; Score 37; DB 16; Length 103;
Best Local Similarity 83.3%; Pred. No. 1.5e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6

Db 29 ADWSWA 34
|||||:
|||||:

Search completed: April 26, 2004, 13:13:10
Job time : 182 secs

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